

[NCBI](#)[Entrez](#)[BLAST 2 sequences](#)[BLAST](#)[Example](#)[Help](#)

## BLAST 2 SEQUENCES

This functionality is now available in the main BLAST pages and this link will be removed in the near future. Step-by-step [instructions](#) for use are available.

This tool produces the alignment of two given sequences using BLAST engine for local alignment.

The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from [NCBI ftp site](#)

Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program  blastn  Matrix  Not Applicable

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch:

Use Mega BLAST Strand option  View option

Masking character option  Masking color option

Show CDS translation

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter  Align

Sequence 1

Enter accession, GI or sequence in FASTA format from  to

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtgggtgtca  
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga  
gaaatcttg gtgtttcgc ttttggact caaaagtatg tccagaaaaat  
cccagcgct tttctgagta gatatctgtt ttagcttatac cttaaagagac  
tccttccggc cctggattac tttctctgtg aactgatgaa gttcttggtt  
aaatttagaa aagatttggc cttgagagact gaatttggaaa accaggtcgat
```

or upload FASTA file

Sequence 2

Enter accession, GI or sequence in FASTA format from  to

H21976

or upload FASTA file

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x\_dropoff: 0 expect: 10.000 wordsize: 11 Filter  View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

 Show CDS translation

Sequence 1: lcl|1

Length = 379

Sequence 2: gi|890671|yl38c11.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:160532 5' similar to SP:CP4B\_RABIT P15128 CYTOCHROME P450 IVB1 ;, mRNA sequence.

Length = 332

No significant similarity was found

CPU time: 0.04 user secs. 0.04 sys. secs 0.08 total secs.

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Program  blastn  Matrix  Not Applicable

Parameters used in BLASTN program only:

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Use Mega BLAST Strand option  View option

Masking character option  Masking color option

Show CDS translation

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter  Align

Sequence 1

Enter accession, GI or sequence in FASTA format from  to

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtgggtgtca  
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga  
gaaatcttg gtgtttcgc ttttggact caaaagtatg tccagaaaaat  
cccagcgct tttctgagta gatatctgtt ttagcttatac cttaaagagac  
tccttccggt cctggattac tttctctgtg aactgatgaa gttcttggtt  
aaatttagaa aagatttggc cttgagagact gaatttggaaa accaggtcgat
```

or upload FASTA file

Sequence 2

Enter accession, GI or sequence in FASTA format from  to

```
H21977
```

or upload FASTA file

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x\_dropoff: 0 expect: 10.000 wordsize: 11 Filter  View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

 Show CDS translation

Sequence 1: lcl|1

Length = 379

Sequence 2: gi|890672|y|38c11.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:160532 3', mRNA sequence.

Length = 444

No significant similarity was found

CPU time: 0.03 user secs. 0.01 sys. secs 0.04 total secs.

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Program  blastn  Matrix  Not Applicable

Parameters used in BLASTN program only:

Reward for a match:  Penalty for a mismatch:

Use Mega BLAST Strand option  View option

Masking character option  Masking color option

Show CDS translation

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter  Align

Sequence 1

Enter accession, GI or sequence in FASTA format from  to

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtgggtgtca  
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga  
gaaatcttg gtgtttcgc ttttggact caaaagtatg tccagaaaaat  
cccagcgct tttctgagta gatatctgtt ttagcttatac cttaaagagac  
tccttccggc cctggattac tttctctgtg aactgatgaa gttcttggtt  
aaatttagaa aagatttggc cttgagagact gaatttggaaa accaggtcgat
```

or upload FASTA file

Sequence 2

Enter accession, GI or sequence in FASTA format from  to

H25577

or upload FASTA file

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x\_dropoff: 0 expect: 10.000 wordsize: 11 Filter  View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

Show CDS translation Align

Sequence 1: lcl|1

Length = 379

Sequence 2: gi|894700|y|48g04.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:161526 3', mRNA sequence.

Length = 421

No significant similarity was found

CPU time: 0.04 user secs. 0.03 sys. secs 0.07 total secs.

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Program  Matrix

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

Use Mega BLAST Strand option  View option

Masking character option  Masking color option

Show CDS translation

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter  Align

Sequence 1

Enter accession, GI or sequence in FASTA format from  to

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtgggtgtca  
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga  
gaaatcttg gtgtttcgc ttttggact caaaagtatg tccagaaaaat  
cccagcgct tttctgagta gatatctgtt ttagcttatac cttaaagagac  
tccttccggt cctggattac tttctctgtg aactgatgaa gttcttggtt  
aaatttagaa aagatttggc cttgagagact gaatttggaa accaggtcgat
```

or upload FASTA file

Sequence 2

Enter accession, GI or sequence in FASTA format from  to

H25624

or upload FASTA file

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x\_dropoff: 0 expect: 10.000 wordsize: 11 Filter  View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

 Show CDS translation Align

Sequence 1: lcl|1

Length = 379

Sequence 2: gi|894747|lyl48g04.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:161526 5' similar to gb:J02871 CYTOCHROME P450 IVB1 (HUMAN);contains Alu repetitive element;, mRNA sequence.

Length = 432

No significant similarity was found

CPU time: 0.04 user secs. 0.03 sys. secs 0.07 total secs.

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Program  blastn  Matrix  Not Applicable

Parameters used in BLASTN program only:

Reward for a match: Penalty for a mismatch:

Use Mega BLAST Strand option  View option

Masking character option  Masking color option

Show CDS translation

Open gap  and extension gap  penalties

gap x\_dropoff  expect  word size  Filter  Align

Sequence 1

Enter accession, GI or sequence in FASTA format from  to

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtgggtgtca  
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga  
gaaatcttg gtgtttcgc ttttggact caaaagtatg tccagaaaaat  
cccagcgct tttctgagta gatatctgtt ttagcttatac cttaaagagac  
tccttccggc cctggattac tttctctgtg aactgatgaa gttcttggtt  
aaatttagaa aagatttggc cttgagagact gaatttggaaa accaggtcgat
```

or upload FASTA file

Sequence 2

Enter accession, GI or sequence in FASTA format from  to

```
AA003705
```

or upload FASTA file

Comments and suggestions to [blast-help@ncbi.nlm.nih.gov](mailto:blast-help@ncbi.nlm.nih.gov)



## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x\_dropoff: 0 expect: 10.000 wordsize: 11 Filter  View option Standard

Masking character option X for protein, n for nucleotide Masking color option Black

 Show CDS translation

Sequence 1: lcl|1

Length = 379

Sequence 2: gil1447205|mg61a02.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone  
IMAGE:437450 5', mRNA sequence.

Length = 331

No significant similarity was found

CPU time: 0.02 user secs. 0.03 sys. secs 0.05 total secs.